3. (As Twice Amended) An isolated polynucleotide encoding a polypeptide selected from the group consisting of:

a) a polypeptide comprising the amino acid sequence of SEQ ID NO:1,

b) a polypeptide comprising a naturally-occurring amino acid sequence at least 90% identical to the amino acid sequence of SEQ ID NO:1, and

c) a fragment of a polypeptide having the amino acid sequence of SEQ ID NO:1, wherein said fragment transports phosphate.

4. (As Once Amended) An isolated polynucleotide of claim 3, encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:1.

5. (As Once Amended) An isolated polynucleotide of claim 3, comprising the polynucleotide sequence of SEQ ID NO:2.

6. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 3.

7. A cell transformed with a recombinant polynucleotide of claim 6.

9. A method of producing a polypeptide encoded by the polynucleotide of claim 3, the method comprising:

a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide, and said recombinant polynucleotide comprises a promoter sequence operably linked to the polynucleotide of claim 3, and

b) recovering the polypeptide so expressed.

10. (As Once Amended) The method of claim 9, wherein the polypeptide has the amino acid sequence of SEQ ID NO:1.

12. (As Once Amended) An isolated polynucleotide selected from the group consisting of:

a) a polynucleotide comprising the polynucleotide sequence of SEQ ID NO:2,

b) a polynucleotide comprising a naturally-occurring polynucleotide sequence at least 90% identical to the polynucleotide sequence of SEQ ID NO:2,

c) a polynucleotide completely complementary to a polynucleotide of a),

d) a polynucleotide completely complementary to a polynucleotide of b), and

e) an RNA equivalent of a)-d).

13. (As Twice Amended) An isolated polynucleotide comprising at least 20 contiguous nucleotides of a polynucleotide selected from the group consisting of:

a) a polynucleotide consisting of nucleotides 1183 through 1454 of the polynucleotide sequence of SEQ ID NO:2,

b) a polynucleotide consisting of a naturally-occurring polynucleotide sequence at least 90% identical to nucleotides 1183 through 1454 of the polynucleotide sequence of SEQ ID NO:2,

c) a polynucleotide completely complementary to a polynucleotide of a),

d) a polynucleotide completely complementary to a polynucleotide of b), and

e) an RNA equivalent of a)-d).

14. A method of detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 12, the method comprising:

a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and

b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

15. The method of claim 14, wherein the probe comprises at least 60 contiguous nucleotides.

16. A method of detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 12, the method comprising:

a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and

b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amout thereof.

28. A method of screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim 5, the method comprising:

a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,

b) detecting altered expression of the target polynucleotide, and

c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

29. A method of assessing toxicity of a test compound, the method comprising:

a) treating a biological sample containing nucleic acids with the test compound,

b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 12 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 12 or fragment thereof,

c) quantifying the amount of hybridization complex, and

d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

46. A microarray wherein at least one element of the microarray is a polynucleotide of claim 13.

47. A method of generating a transcript image of a sample which contains polynucleotides, the method comprising:

a) labeling the polynucleotides in the sample,

b) contacting the elements of the microarray of claim 46 with the labeled polynucleotides of the sample under conditions suitable for the formation of a hybridization complex, and

c) quantifying the expression of the polynucleotides in the sample.

48. (Twice Amended) An array comprising different nucleic acid molecules affixed in distinct physical locations on a solid substrate, wherein at least one of said nucleic acid molecules comprises a first oligonucleotide or polynucleotide sequence completely complementary to at least 30 contiguous nucleotides of a target polynucleotide, and wherein said target polynucleotide is a polynucleotide of claim 12.

57. (As Twice Amended) A polynucleotide of claim 12, selected from the group consisting of:

a) a polynucleotide comprising the polynucleotide sequence of SEQ ID NO:2,

b) a polynucleotide comprising a naturally-occurring polynucleotide sequence at least 95% identical to the polynucleotide sequence of SEQ ID NO:2,

c) a polynucleotide completely complementary to a polynucleotide of a),

d) a polynucleotide completely complementary to a polynucleotide of b), and

e) an RNA equivalent of a)-d).

58. (As Once Amended) An isolated polynucleotide of claim 13, comprising at least 60 contiguous nucleotides of a polynucleotide selected from the group consisting of:

a) a polynucleotide consisting of nucleotides 1183 through 1454 of the polynucleotide sequence of SEQ ID NO:2,

b) a polynucleotide consisting of a naturally-occurring polynucleotide sequence at least 90%

identical to nucleotides 1183 through 1454 of the polynucleotide sequence of SEQ ID NO:2,

c) a polynucleotide completely complementary to a polynucleotide of a),

d) a polynucleotide completely complementary to a polynucleotide of b), and

e) an RNA equivalent of a)-d).

59. An isolated polynucleotide of claim 13, comprising at least 20 contiguous nucleotides of a polynucleotide selected from the group consisting of:

a) a polynucleotide consisting of the polynucleotide sequence of SEQ ID NO:5,

b) a polynucleotide completely complementary to a polynucleotide of a), and

c) an RNA equivalent of a)-b).